

Amendments to the Specification:

Replace the paragraph beginning at page 6, line 32 as with the following amended paragraph:

Polynucleotide or polypeptide sequences may be aligned, and percentage of identical nucleotides in a specified region may be determined against another sequence, using computer algorithms that are publicly available. Two exemplary algorithms for aligning and identifying the similarity of polynucleotide sequences are the BLASTN and FASTA algorithms. The similarity of polypeptide sequences may be examined using the BLASTP algorithm. Both the BLASTN and BLASTP software are available on the NCBI anonymous FTP server (~~ftp://ncbi.nlm.nih.gov~~) ~~under /blast/executables/~~. The BLASTN algorithm version 2.0.4 [Feb-24-1998], set to the default parameters described in the documentation of variants according to the present invention. The use of the BLAST family of algorithms, including BLASTN and BLASTP, is described at NCBI's website at ~~URL http://www.ncbi.nlm.nih.gov/BLAST/newblast.html~~ and in the publication of Altschul, Stephen F., *et al.* (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", *Nucleic Acids Res.* 25:3389-34023. The computer algorithm FASTA is available on the Internet at ~~the an ftp site of the University of Virginia ftp://ftp.virginia.edu/pub/fasta/~~. Version 2.0u4, February 1996, set to the default parameters described in the documentation and distributed with the algorithm, is also preferred for use in the determination of variants according to the present invention. The use of the FASTA algorithm is described in W. R. Pearson and D. J. Lipman, "Improved Tools for Biological Sequence Analysis", *Proc. Natl. Acad. Sci. USA* 85:2444-2448 (1988) and W. R. Pearson, "Rapid and Sensitive Sequence Comparison with FASTP and FASTA, " *Methods in Enzymology* 183:63-98 (1990).

Replace the paragraph beginning at page 14, line 20 as with the following amended paragraph:

The novel superantigens were identified by searching the *S. pyogenes* M1 genome database at the University of Oklahoma (~~http://www.genome-ou.edu/strep.html~~) with highly conserved $\beta 5$

Applicant : John D. Fraser, et al.

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and $\alpha 4$ regions of streptococcal and staphylococcal superantigens, using a TBlastN search programme.
